

# FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC  
TGTGCCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT  
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCGGC  
GTTTGGCCCAGGACGGGGCCCATGTGGTCGTCAGCAGCCGGAAGCAGCAGAATGTGGACCAG  
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA  
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC  
TAGTCTCCAATGCTGCTGTCAACCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG  
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC  
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC  
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAACAGCCTTGCTGGGCCTGACCAAGACC  
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAACTGCCTAGCACCTGGACTTATCAA  
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC  
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCCTGTGCTCT  
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT  
CTGAGGACCGGGAGACAGCCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCTCTGC  
ATTCACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT  
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTCTGCT  
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT  
GAGTCTACCTTGGCAAAGACCAAGATATTTTTTCTGGGCCACTGGTGAATCTGAGGGGTGA  
TGGGAGAGAAGGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG  
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

## **FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVS  
SRKQQNVNQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG  
SIMDVTEEVWDKTLNINVKAPALMTKAVVPEMEKRGSGSVVIVSSIAAFSPSPGFSPYNVSK  
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC  
AGIVSFLCSEDASYITGETVVVGGGTPSRL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation site.**

amino acids 183-186

**N-myristoylation sites.**

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 276-278

# FIGURE 3

GCGCCCTGAGCTCCGCCTCCGGGCCCCGATAGCGGCATCGAGAGCGCCTCCGTCGAGGACCAGGCGGCG  
CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCTGCAGAACCAGGTGGC  
GCGGCTGGAGGAGGAGAACCGAGACTTTCTGGCTGCGCTGGAGGACGCCATGGAGCAGTACAAACTGC  
AGAGCGACCGGCTGCGTGAGCAGCAGGAGGAGATGGTGGAACCTGCGGCTGCGGTTAGAGCTGGTGCGG  
CCAGGCTGGGGGGGCTGCGGCTCCTGAATGGCCTGCCTCCCGGGTCCTTTGTGCCTCGACCTCATAC  
AGCCCCCTGGGGGGGTGCCACGCCCATGTGCTGGGCATGGTGCCGCCTGCCTGCCTCCCTGGAGATG  
AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT  
GAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGAGCCGCC  
CAGGCGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGGCACGCCAG  
GGAGTCTGCCAGAGAGGAAGGGCCCAGAGCTTTGCCTTGAGGAGTTGGATGCAGCCATTCCAGGGTCC  
AGAGCAGTTGGTGGGAGCAAGGCCCGAGTTCAGGCCCGCCAGGTCCCCCTGCCACAGCCTCAGAGTG  
GCGGCTGGCCCAGGCCAGCAGAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA  
TTGGCGAGCTGGTCCGCACAGGAAGGCAGCTCAGGCCCTGAACCGCCAGCACAGCCAGCGTATCCGG  
GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCAGCTGCGGGAGCT  
CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTTCCGCAGGAGGGTTCGCTG  
CGGCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTGTCACTGTCTG  
GCCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGCAGGGACA  
GCTGCAGAGGCGGCTTCGCGAGGAGACGGAGCAGAAGCGGCGCCTGGAGGCAGAAATGAGCAAGCGGC  
AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATTAAGACGGAA  
GAGATCGCGGCCTTCCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTCAGCCTGGAACAGCA  
GCAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAGCGGCGGG  
CGCTGGAGGAGCTGGGGGAGGAGCTCCACAAGCGGGAGGCCATCCTGGCCAAGAAGGAGGCCCTGATG  
CAGGAGAAGACGGGGCTGGAGAGCAAGCGCCTGAGATCCAGCCAGGCCCTCAACGAGGACATCGTGCG  
AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGCTGCGGCAGGGCA  
GCGCCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGCTGCTC  
AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGGAGTCTGCTGTCCCCGAGGAGGAGCGGAC  
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA  
CATGCCGCCAGCGGGTGCTTCGGGCCTCAGCCTCGTTGCTGTCCAGTGCGAGATGAACCTCATGGCC  
AAGCTCAGCTACCTCTCATCCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTTGACAAGGTGGTGAC  
GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCTTCTCGGAACTGGAGATGCAGCTGGAGGAGCAGC  
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCCTGGAGATGGACCGCCAGCTGACC  
CTGCAGCAGAAGGAGCACGAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCGAGACCACCTCGGTGA  
AGGGTTAGCAGACAGCAGGAGGCAGTATGAGGCCCGGATTCAAGCTCTGGAGAAGGAACTGGGCCGTT  
ACATGTGGATAAACCAGGAACTGAAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT  
GGGGAGAAGAGGAGCCTGTGCTCGGAGGGCAGACAGGCTCCTGGAAATGAAGATGAGCTCCACCTGGC  
ACCCGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGACGCGGGACT  
TGGTCCACGCTCCGTTACCTTGACCTGGAAACGCTCGAGCCTGTGTGGTGAGGAGCAGGGGTCCCC  
GAGGAACTGAGGCAGCGGGAGGCGGCTGAGCCCTGGTGGGGCGGGTGCTTCCTGTGGGTGAGGCAGG  
CCTGCCCTGGAACTTTGGGCCTTTGTCCAAGCCCCGGCGGGAAGTGCACGAGCCAGCCCGGGGATGA  
TTGATGTCCGGA AAAACCCCTGTAAGCCCTCGGGGCAGACCCTGCCTTGGAGGGAGACTCCGAGCCT  
GCTGAAAGGGGCAGCTGCCTGTTTTGCTTCTGTGAAGGGCAGTCCTTACCGCACACCCTAAATCCAGG  
CCCTCATCTGTACCCTCACTGGGATCAACAAATTTGGGCCATGGCCCAAAGAACTGGACCCTCATTT  
AACAAAATAATATGCAATTTCCACCACTTACTTCCATGAAGCTGTGGTACCCAATTGCCGCCTTGTG  
TCTTGCTCGAATCTCAGGACAATTCTGGTTTTAGGCGTAAATGGATGTGCTTGTAGTTCAGGGGTTTG  
GCCAAGAATCATCACGAAAGGGTCGGTGGCAACCAGGTTGTGGTTTTAAATGGTCTTATGTATATAGGG  
GAAACTGGGAGACTTTAGGATCTTAAAAAACCATTTAATAAAAAAAATCTTTGAAGGGAC

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## **FIGURE 4**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLQSDRLREQQEEMVELRLRLLELVRPGWGGLRLLNGLPPGSFVPRPHTAPLGGAHAHV  
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEEEPPRRTL  
HLRRNRISNCSQRAGARPGSLPERKGPCLCLEELDAI PGSRVGGSKARVQARQVPPATAS  
EWRLAQAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE  
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQVLKEKKQATERLVSLSAQSEKRLQE  
LERNVQLMRQQQGQLQRRRLREETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA  
AFQRKRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQQRRALEELGEELHKREAILAKKE  
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAAQSQQQIRGEIDS  
LRQEKDSLKQRLEIDGKLRQGSLLSPEEERTLFQLDEAIEALDAAIEYKNEAITCRQRVLR  
ASASLLSQCEMNLMAKLSYLSSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLLEEQQR  
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRQYEARIQALEK  
ELGRYMWINQELKQKLGGVNAVGHSGGGEKRSLCSEGRQAPGNEDELHLAPELLWLSPLTEG  
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG  
PLSKPRRELRRASPGMIDVRKNPL

### **Important features:**

#### **Leucine zipper pattern.**

amino acids 557-579, 794-815

#### **N-glycosylation sites.**

amino acids 133-136, 383-386

#### **Kinesin related protein Kif-4 Coiled-coil domain:**

amino acids 231-672

## **FIGURE 5**

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT  
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA  
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG  
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT  
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG  
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACCTTATCTCCCATCTCCCGGAGCTGTAC  
CAGGAACAGGAGGCACGTCCTGTACCCATTAAAAACCCCAGGCTCCACTGGCAGACGGCAGAC  
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA  
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC  
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTCCAGCTCCCCTTCCCGCTGAG  
AGCCACTTTCATCGGCAATAAAATCCCCCACATTTACCATCT

## FIGURE 6

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700
```

><subunit 1 of 1, 125 aa, 1 stop

><MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFL LQCSKGT TDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAILS

LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRSCTRNRRHVLYP

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	35.2	12.5	20	65
Gender	0.45	0.50	0	1
Marital Status	0.65	0.48	0	1
Education	12.5	2.5	9	16
Income	45000	15000	20000	80000
Health	0.75	0.42	0	1
Smoking	0.35	0.48	0	1
Alcohol	0.25	0.43	0	1
Exercise	0.55	0.50	0	1
Stress	0.60	0.49	0	1
Depression	0.30	0.46	0	1
Loneliness	0.40	0.49	0	1
Social Support	0.70	0.45	0	1
Life Satisfaction	0.65	0.47	0	1
Quality of Life	0.70	0.46	0	1
Physical Health	0.75	0.42	0	1
Mental Health	0.60	0.49	0	1
Overall Health	0.68	0.47	0	1

## FIGURE 7

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT  
TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG  
AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCG  
GAGAAGCGGGGACGAGGCCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT  
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCCG  
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGG  
TCGCCGGCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCCGCTGCTACCCCTG  
CGCCCGCTGCGAGCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG  
GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCCGCC  
GCCCGCCGGGACGTGGTAGGGGATGCCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA  
GTTCCCTCCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG  
AAGCTGGCCCAGGCACCAGAGCAGCCGGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG  
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT  
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC  
TGGGTCTCCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACAC  
CCCGCAGGCGGAAGCCCTGGCCGCAGCCGCCCAGGACGCGATTGGCCCCGGA ACTCGCGCCCA  
CGCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG  
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCT  
GTGCACCGAGGAGGGGCCGCTGTGCGCGCAGCCCGAGTGCCCCGAGGCTGCACCCGCGCTGCA  
TCCACGTCGACACGAGCCAGTGCTGCCCGCAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC  
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTG  
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACC  
CTGTGTACGAGCCTGATCAGTGCTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAA  
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTAC  
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC  
AAATGTAGACGCTTCCCAGAACACAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAA  
CATTCTAGATGACTCTGGGAACTATCAGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAA  
TTGTTGGTACTTTTCCTTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTT  
AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACAG  
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG  
CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTCAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

><MW: 35296, pI: 5.37, NX(S/T): 0

MPSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL  
GRPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDT PQAEALA  
AAQDAIGPELAPTPEPP E EYVYPDYRGKGCVDESGFVYAIG EK FAPGPSACPC LCTEEGPL  
CAQPEC PRLHPRCIHV DTSQCCPQCKERKNYCEFRGKTYQTLEEFV VSPCERCRC EANGEVL  
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVK TDECTICHCTYE EGTWR  
IERQAMCTRHECRQM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site.**

amino acids 80-83

**N-myristoylation sites.**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence.**

amino acids 114-117

**EGF-like domain cysteine pattern signature.**

amino acids 176-187



## **FIGURE 9**

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC  
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG  
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC  
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGG  
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT  
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA  
ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAAC  
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATAACGAGATGTGCGAGGTGGGGCAGGT  
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG  
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG  
GTGCTTGTGGCCTCCTATAACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTC  
CTACCTGTGTGCAGCCCCCTTGGAACTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG  
GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAT  
GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCG  
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
GTGGGGAGTGGTTTGCCCTTCCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA  
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC  
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTATATCTACTCACCTAACAGCA  
AACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG  
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

## **FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847

><subunit 1 of 1, 437 aa, 1 stop

><MW: 46363, pI: 6.22, NX(S/T): 3

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLI  
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL  
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 243-260

**N-glycosylation sites.**

amino acids 46-49, 189-192, 382-385

**Glycosaminoglycan attachment sites.**

amino acids 51-54, 359-362

**N-myristoylation sites.**

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,  
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,  
360-365, 361-366, 388-393, 408-413, 419-424

## FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGGCCCTG  
GCTGCGGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGC  
CTCGTCGCTCAGCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT  
TGTCGGGGCCCCGAGGCTCCGTGGCGGGACCCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG  
CAGCTGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT  
GAGGCAGCTGCACGGGTTGCTGCAGGCCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCG  
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC  
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CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGC  
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AGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATG  
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CTCGAACCTGATATTTGTGCTTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAATTCC  
GAGTGCAGATGTTATTAAATGAAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCA  
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ACAGGAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTC  
TCTGGGTTTGGACATGAAATGTAAGAAAAGATTTTTTCACTGGAGCAGCTCTCTTAAGGAGAA  
ACAAATCTATTTAGAGAAACAGCTGGCCCTGCAAATGTTTACAGAAATGAAATTCTTCCTAC  
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTTCATAATAACACTTGAAAAGTGCT  
GGAGTAACAAAATATCTCAGTTGGACCATCCTTAACCTTGATTGAACTGTCTAGGAACTTTAC  
AGATTGTTCTGCAGTTCTCTCTTTCTTTCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC  
AGGAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT  
TTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAA  
TGAAAATAAATATTTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCCTT  
TTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATATGTTTGGACAATTAGCAAC  
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTTCATTCTGT  
CACTTGGCTTCGATTTTTTATATTTTCCTATTATATGAAATGTATCTTTTGGTTGTTTGATTT  
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA  
TAAAGAAAATTCTTGTGACTTTAAAAA

## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSFYFGTKTRYEDVNPVLLS  
GPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS  
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR  
CMDSSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH  
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA  
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE  
TLLPLLSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV  
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

### **Important features:**

#### **Signal sequence**

amino acids 1-30

#### **N-glycosylation sites.**

amino acids 242-246, 481-485

#### **N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

#### **Endoplasmic reticulum targeting sequence.**

amino acids 484-489

## FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAAGTGTCTTGCATCATTACGGATTTCGC  
AGACAAGTGACCCAGGATCGAGTGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT  
CCAGAGCCAATCCCAGATTTTCGAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTTCCTGCTG  
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTGTCTTGTCTGTACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAAGCTTTTCGTTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCCTGAGTTGGGTTCCCTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGCTCACGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTTACCCTGGTCTGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCTGAGTGTCCATTGTGGAGAAGCTTTTTGGATCAGCATTTTGTAACAAACCAAAATCAGGAAG  
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT  
TACATCTAAATTTTTGCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT  
CATACAATGTTAAATAACCTATTTTTTTTAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT  
TGGAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTTCTTTTCT  
CACACAAGTTTTAGCCTTTTTTACAAGGGAACCTCACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAATTATTTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT  
CCCCTGTTCTTCTTGGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG  
TGAAACGCCTGAATCAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTTCATCCGCCGGAGACACTGCTCCCAT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTTCTAGCTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTATAGTAGGGTAGCCTTATTGCCCCCTCTTCTTATACCTAAACCTTCTACACTAGTGCCA  
TGGAACAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTGTGTTAAC  
CTCATTTATAAAAGCTTCAAAAAAACCCA

## **FIGURE 14**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS�KIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIGGIIGG  
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

## FIGURE 15

CAGGACCAGGTCTTCCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG  
ATCCTGCTGACGCTGGGCCCCGCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTTCCGGAG  
GAGAAGCCACTGCCCACCGCCTTCCTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCTGACTGGCTGAAGCTG  
CGCATGATCCGTTCTGAGGTGCTCCGCCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCAGCAGCTGCTGCTG  
TTCGTGCAGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAATCCTCCAGTTCTTGGACCAGGCAGTGGCCAC  
GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCACCTGGTGGAGGTCCAGCATGAGCGC  
GGCGCCTCCGGAGGCCAGACTTTCCACTCCTTGCTCACAGCCTCCCTGCCGCCCCGCCGAGACAGCACAGAGGCA  
CCCAAACCAAAGAGCAGCCAGAGCAGCCCATAGGCCAGGGCCGGATTCCGGTGGGGACCCAGCTCCGGGTGCTG  
GGCCTGAGGACGACCTGGCTGGCATGTTCTCCAGATTTTCCCGCTCAGCCCGGACCCTCGGTGGCAGAGCTCC  
AGTCCCCGCCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCGCGTCTGCCAGGGCAGCCCC  
GAGGTGCCGGGCATCACGGTGCCTGCTGCTGAGGCCCTCGCCACCCTGCTCAGCTCCCCACACGGCGGTGCCCTG  
GTGATGTCCATGCACCGTAGCCACTTCCTGGCCTGCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCGCTGTGTG  
CCACAGGACACCGGCTTCTCCTCGCTCTTCTGAAGGTGCTCCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC  
GTGGAGGGCGGGCCCCCTGCGGGCACAGCTCAGGATGCTTGCCAGCCAGGCCCTCAGCCGGGCGCAGGCTCAGTGAT  
GTGCGAGGGGGGCTCCTGCGCCTGGCCGAGGCCCTGGCCTTCCGTGAGGACCTGGAGGTGGTTCAGCTCCACCGTC  
CGTGCCGTCTATCGCCACCCTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCCGGACCTGATCAGCAAAGTCTCCAG  
GGGCTGATCGAGGTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTTCTCTGCCACTGCGGATGCTGCC  
TCCCCGTTTCCAGCCTGTAAGCCCCGTTGTGGTGGTGGAGCTCCCTGCTGCTGCAGGAGGAGGAGCCCCCTGGCTGGG  
GGGAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCCCTCGTCAGGCCTCCTAGTGGACTGG  
CTGGAAATGCTGGACCCCCGAGGTGGTTCAGCAGCTGCCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGGAGGAAG  
GGCAAAGGTGAGGCCAGGTGCCCTCGTTCCGTCCCTACCTCCTGACCCTCTTACGCATCAGTCCAGCTGGCCC  
ACACTGCACCAGTGCATCCGAGTCTTGCTGGGCAAGAGCCGGGAACAGAGGTTTCGACCCCTCTGCCTCTCTGGAC  
TTCTCTGCGCCTGCATCCATGTTCTCCTCGCATCTGGCAGGGGGCGGGACCAGCGCACCCCGCAGAAGCGGCGGGAG  
GAGCTGGTGTGCGGGTCCAGGGCCCCGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCGG  
AGCCAGGACGGGGACACAGCCGCCCTGCAGCCTCATCCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG  
GACGATGAGAGTGTGAGGAAGGTGACGGAGCACCTGTGAGGCTGCATCCAGCAGTGGGGAGACAGCGTGCTGGGA  
AGGCGCTGCCGAGACCTTCTCCTGCAGCTCTACCTACAGCGGCCGGAGCTGCGGGTGCCCGTGCTGAGGTCTTA  
CTGCACAGCGAAGGGGCTGCCAGCAGCAGCGTCTGCAAGCTGGACGGACTCATCCACCGCTTCATCACGCTCCTT  
GCGGACACCAGCGACTCCCGGGCGTTGGAGAACCGAGGGGGCGGATGCCAGCATGGCCTGCCGGAAGCTGGCGGTG  
GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCCTGCACGGCCGCACCCACCTCAACTTC  
CAGGAGTTCCGGCAGCAGAACCACCTGAGCTGCTTCTGACGTGCTGGGCCTGCTGGAGCTGCTGCAGCCGCAC  
GTGTTCCGCGAGCGAGCACCAGGGGGCGCTGTGGGACTGCCTTCTGTCTTCATCCGCCTGCTGCTGAATTACAGG  
AAGTCTTCCCGCCATCTGGCTGCCTTCATCAACAAGTTTGTGAGTTTCATCCATAAGTACATTACCTACAATGCC  
CCAGCAGCCATCTCCTTCTGAGAACGACGCGGCCGCTCCACGACCTGTCTTTCGACAACAGTGACCTGGTG  
ATGCTGAAATCCCTCCTTGCAGGGCTCAGCCTGCCAGCAGGGACGACAGGACCGACCGAGGCCTGGACGAAGAG  
GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGCCCCCTGGTCAGCGTCTCCCTGTTTACCCCTCTGACCGCGGCCGAG  
ATGGCCCCCTACATGAAACGGCTTTCCCGGGGGCCAAACGGTGGAGGATCTGCTGGAGGTCTGAGTGACATAGAC  
GAGATGTCCCGGCGGAGACCCGAGATCCTGAGCTTCTTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG  
GAGTGTTGCCGCAACCTCGCCTTCAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTTC  
CTGCCCACGTTTCATGTACTGCCTGGGCAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCTGAG  
TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGGCCTTCTGGTGGGCATGTACGGCCAGATG  
GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATGTGAGCCCTGTGGCAGCCGA  
CCCCCTCCAAGCCCCGGCCCGTCCCGTCCCCGGGGATCCTCGAGGCAAAGCCAGGAAGCGTGGGCGTTGCTGG  
TCTGTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGCAGGCCAGGAGCAATACTCCGAGCCCTGGGGTGG  
CTCCGGGCGGGCGCTGGCATCAGGGGCGGTCCAGCAAGCCCTCATTACCTTCTGGGCCACAGCCCTGCCGCGG  
AGCGGCGGATCCCCCGGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAACTGTCAA

## **FIGURE 16**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRLM  
IRSEVLRLVDAALQDLEPQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY  
MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG  
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL  
ATLLSSPHGGALVMSMHRSHFLACPLLRQLCQYQRCVPQDTGFSSFLKVLQMLQWLDSFG  
VEGGPLRAQLRMLASQASAGRRLSDVRGGLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ  
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASFPACKPVVVVSSLLLQEEEPLA  
GGKPGADGGSLEAVRLGPSSGLLDVWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR  
PYLLTLFTHQSSWPTLHQCIQIRVLLGKSREQRFDPASLDFLWACIHVPRIWQGRDQRTPOKR  
REELVLRVQGPPELISLVELILAEAEATRSQDGDAAACSLIQARLPLLLSCCGDDESVRKVTE  
HLSGCIQQWGDVSVLGRRCRDLLLQLYLQRPPELRVPVPEVLLHSEGAASSSVCKLDGLIHRFI  
TLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLPMAALLHGRTHLNFQEFRQQNHL  
SCFLHVLGLLELLQPHVFRSEHQGALWDCLLSFIRLLLNYRKSSRHAAAFINKFVQFIHKYI  
TYNAPAAISFLQKHADPLHDLSDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG  
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSDIDEMSRRRPEILSFFSTNLQRL  
MSSAECCRNLAFLSLALRSMQNSPSIAAAFLPTFMYCLGSQDFEVVQTALRNLPYALLCQE  
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

#### **N-myristoylation sites.**

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,  
665-671, 698-704

#### **Amidation sites.**

amino acids 329-333, 634-638





## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLLLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDR LHAAEQESLKRSK  
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA  
KESSLQPAVRVGQGRTGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE  
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVVRWRTKQNLD  
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL  
DLSSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSL FQHVGTH  
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGD  
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRTATLRYPRS  
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

### **Important features:**

#### **Signal sequence**

amino acids 1-23

#### **N-glycosylation sites.**

amino acids 5-9, 87-91, 103-107, 465-469

#### **N-myristoylation sites.**

amino acids 6-12, 136-142, 370-376, 509-515